

Sequence Listing

Sequence Listing

5 <110> Chen, Jian
 Filvaroff, Ellen
 Goddard, Audrey
 Gurney, Austin
 Li, Hanzhong
 Wood, William I.

10 <120> IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
 THEREOF

15 <130> P1381-R1

<141> 1999-05-14

20 <150> US 60/085,579
 <151> 1998-05-15

<150> US 60/113,621
 <151> 1998-12-23

25 <160> 26

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 <212> PRT
 <213> Homo sapiens

30 <400> 1
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35 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
 35 40 45

40 Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
 50 55 60

45 Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
 65 70 75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
 80 85 90

Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
 95 100 105
 5 Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
 110 115 120
 Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
 125 130 135
 10 Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg
 140 145 150
 Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln
 15 155 160 165
 Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe
 170 175 180
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 <213> Homo sapiens
 25 <400> 2
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 30 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggg gtcacggatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggg 250
 35 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 40 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgcg ccgccgcctc 500
 45 tgcccgccac cgcccgcac agggccttgc cgccagcgcg cagtcatgga 550
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600

gccaggccag cagcccgaga ccatactcct tgcacctttg tgccaagaaa 650

ggcctatgaa aagtaaacac tgacttttga aagcaag 687

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<210> 3

<211> 197

<212> PRT

<213> Homo sapiens

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<400> 3

Met	Thr	Leu	Leu	Pro	Gly	Leu	Leu	Phe	Leu	Thr	Trp	Leu	His	Thr
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15

Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser
				20					25					30

20

His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly
				35					40					45

Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln
				50					55					60

25

Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His
				65					70					75

Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val
				80					85					90

30

Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser
				95					100					105

Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr
				110					115					120

35

Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile
				125					130					135

40

Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg
				140					145					150

Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg
				155					160					165

45

Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr
				170					175					180

Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val Leu Pro Arg
 185 190 195

Ser Val
 197

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<210> 4

<211> 1047

<212> DNA

10 <213> Homo sapiens

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15 tgacgctcct ccccggcctc ctgtttctga cctggctgca cacatgctg 100

gccaccatg acccctcct cagggggcac cccacagtc acggtacccc 150

20 aactgctac tcggctgagg aactgcccct cggccaggcc cccccacacc 200

tgctggctcg aggtgccaaag tgggggcagg ctttgctgt agccctgggtg 250

tccagcctgg aggcagcaag ccacaggggg aggcacgaga ggccctcagc 300

25 tacgaccag tgcccgggtgc tgcggccgga ggagggtgtg gaggcagaca 350

cccaccagcg ctccatctca ccctggagat accgtgtgga cacggatgag 400

30 gaccgctatc cacagaagct ggccttcgcc gagtgctgt gcagaggctg 450

tategatgca cggacgggce gcgagacagc tgcgctcaac tccgtgcggc 500

tgctccagag cctgctgggtg ctgcgccgcc ggccctgctc ccgcgacggc 550

35 tcggggctcc ccacacctgg ggcctttgcc ttccacaccg agttcatcca 600

cgccccgctc ggctgcacct gcgtgctgcc ccgttcagtg tgaccgccga 650

40 ggccgtgggg cccctagact ggacacgtgt gctccccaga gggcaccccc 700

tatttatgtg tatttattgt tatttatatg cctcccccaa cactaccctt 750

ggggtctggg cattccccgt gtctggagga cagcccccca ctgttctcct 800

45 catctccagc ctcagtagtt gggggtagaa ggagctcagc acctcttcca 850

gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt accttggctc 900

cctgtcctgc tcccggcttc ccttacccta tcaactggcct caggccccgc 950

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5 tatttaagtg tacgtgtatt attaaactga tgaacacatc cccaaaa 1047

<210> 5

<211> 830

<212> DNA

10 <213> Homo sapiens

<220>

<221> unknown

<222> 105-115

15 <223> unknown base

<400> 5

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20 cctggttctt gctccttggg actctgggac ttacaccagt ggcacccttg 100

gctcnnnnnn nnnnnaattc ggtacgaggc tggggttcag gcgggcagca 150

25 gctgcaggct gaccttgcag cttggcgga tggactggcc tcacaacctg 200

ctgtttcttc ttaccatttc catcttcttg gggctgggccc agcccaggag 250

ccccaaaagc aagaggaagg ggcaagggcg gcctgggccc ctgggtccctg 300

30 gccctcacca ggtgccactg gacctggtgt cacggatgaa accgtatgcc 350

cgcattggagg agtatgagag gaacatcgag gagatgttgg ccagactgag 400

35 gaacagttca gagctggccc agagaaagtg tgaggtcaac ttgcagctgt 450

ggatgtccaa caagaggagc ctgtctccct ggggctacag catcaaccac 500

gaccccagcc gtatccccgt ggacctccgg aggcacggtg cctgtgtctg 550

40 ggcttgtgtg aacccttca ccatgcagga ggaccgcagc atgggtgagcg 600

tgccgggtgtt cagccagggt cctgtgcgcc gccgcctctg cccgccaccg 650

45 ccccgcacag ggccttgccg ccagcgcgca gtcattggaga ccatcgctgt 700

gggctgcacc tgcattcttc gaatcgacct ggcccagaag ccaggccagc 750

agcccagagac catcctcctt gcacctttgt gccaaagaaag gcctatgaaa 800

agtaaact gacttttgaa agcaaaaaaa 830

<210> 6

5 <211> 397

<212> DNA

<213> Artificial

<220>

10 <221> unknown

<222> 10, 150, 267

<223> unknown base

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ctcacaacct gctgtttctt cttaccattt ccatcttctt ggggctgggc 100

20 agccaggagc cccaaaagca agaggaaggg gcaagggcgg cctgggccc 150

tggcctggcc tcaccaggtg cactggacc tgggtgtcacg gatgaaaccg 200

tatgcccgc tggaggagta tgagaggaac atcgaggaga tgggtggcca 250

25 gctgaggaac agctcanaag ctggcccaga gaaagtgtga ggtcaacttg 300

cagctgtgga tgtccaacaa gaaggagcct gtctcccttg gggctacaag 350

30 catcaaccac cgaccccagc cgtatccccg tgggaccttg ccgggac 397

<210> 7

<211> 230

<212> DNA

<213> Artificial

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<400> 7

cacggatgag gaccgctatc cacagaagct ggccttcgcc gagtgctgt 50

40 gcagaggctg tatcgatgca cggacgggcc gcgagacagc tgcgtcaac 100

tccgtgcggc tgetccagag cctgctgggtg ctgcgccgcc ggccctgctc 150

ccgcgacggc tcggggctcc ccacacctgg ggcctttgcc ttccacaccg 200

45 agttcatcca cgtccccgtc ggctgcacct 230

<210> 8

<211> 24

<212> DNA
 <213> Artificial sequence

<400> 8

5 atccacagaa gctggccttc gccg 24

<210> 9

<211> 24

<212> DNA

10 <213> Artificial sequence

<400> 9

gggacgtgga tgaactcggg gtgg 24

15 <210> 10

<211> 40

<212> DNA

<213> Artificial sequence

20 <400> 10

tatccacaga agctggcctt cgccgagtgc ctgtgcagag 40

<210> 11

<211> 155

25 <212> PRT

<213> Human

<400> 11

30	Met	Thr	Pro	Gly	Lys	Thr	Ser	Leu	Val	Ser	Leu	Leu	Leu	Leu	Leu
	1				5					10					15

	Ser	Leu	Glu	Ala	Ile	Val	Lys	Ala	Gly	Ile	Thr	Ile	Pro	Arg	Asn
					20					25					30

35	Pro	Gly	Cys	Pro	Asn	Ser	Glu	Asp	Lys	Asn	Phe	Pro	Arg	Thr	Val
					35					40					45

	Met	Val	Asn	Leu	Asn	Ile	His	Asn	Arg	Asn	Thr	Asn	Thr	Asn	Pro
					50					55					60

40	Lys	Arg	Ser	Ser	Asp	Tyr	Tyr	Asn	Arg	Ser	Thr	Ser	Pro	Trp	Asn
					65					70					75

45	Leu	His	Arg	Asn	Glu	Asp	Pro	Glu	Arg	Tyr	Pro	Ser	Val	Ile	Trp
					80					85					90

	Glu	Ala	Lys	Cys	Arg	His	Leu	Gly	Cys	Ile	Asn	Ala	Asp	Gly	Asn
					95					100					105

Val Asp Tyr His Met Asn Ser Val Pro Ile Gln Gln Glu Ile Leu
 110 115 120

5 Val Leu Arg Arg Glu Pro Pro His Cys Pro Asn Ser Phe Arg Leu
 125 130 135

Glu Lys Ile Leu Val Ser Val Gly Cys Thr Cys Val Thr Pro Ile
 140 145 150

10 Val His His Val Ala
 155

<210> 12
 15 <211> 408
 <212> PRT
 <213> Artificial

<220>
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25 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val
 30 35 40 45

Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu
 50 55 60

35 Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn
 65 70 75

Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu
 80 85 90

40 Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile
 95 100 105

Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg
 110 115 120

45 Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp
 125 130 135

	Arg Ser Met Val	Ser Val Pro Val Phe	Ser Gln Val Pro Val Arg	
	140		145	150
5	Arg Arg Leu Cys	Pro Pro Pro Pro Arg	Thr Gly Pro Cys Arg Gln	
	155		160	165
	Arg Ala Val Met	Glu Thr Ile Ala Val	Gly Cys Thr Cys Ile Phe	
	170		175	180
10	Pro Asp Lys Thr	His Thr Cys Pro Pro	Cys Pro Ala Pro Glu Leu	
	185		190	195
	Leu Gly Gly Pro	Ser Val Phe Leu Phe	Pro Pro Lys Pro Lys Asp	
15	200		205	210
	Thr Leu Met Ile	Ser Arg Thr Pro Glu	Val Thr Cys Val Val Val	
	215		220	225
20	Asp Val Ser His	Glu Asp Pro Glu Val	Lys Phe Asn Trp Tyr Val	
	230		235	240
	Asp Gly Val Glu	Val His Asn Ala Lys	Thr Lys Pro Arg Glu Glu	
	245		250	255
25	Gln Tyr Asn Ser	Thr Tyr Arg Val Val	Ser Val Leu Thr Val Leu	
	260		265	270
	His Gln Asp Trp	Leu Asn Gly Lys Glu	Tyr Lys Cys Lys Val Ser	
30	275		280	285
	Asn Lys Ala Leu	Pro Ala Pro Ile Glu	Lys Thr Ile Ser Lys Ala	
	290		295	300
35	Lys Gly Gln Pro	Arg Glu Pro Gln Val	Tyr Thr Leu Pro Pro Ser	
	305		310	315
	Arg Glu Glu Met	Thr Lys Asn Gln Val	Ser Leu Thr Cys Leu Val	
	320		325	330
40	Lys Gly Phe Tyr	Pro Ser Asp Ile Ala	Val Glu Trp Glu Ser Asn	
	335		340	345
	Gly Gln Pro Glu	Asn Asn Tyr Lys Thr	Thr Pro Pro Val Leu Asp	
45	350		355	360
	Ser Asp Gly Ser	Phe Phe Leu Tyr Ser	Lys Leu Thr Val Asp Lys	
	365		370	375

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Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 395 400 405

5 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 410 415 420

Leu Ser Pro Gly Lys
 425

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 <211> 212
 <212> PRT
 <213> Homo sapiens

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 1 5 10 15

20 Leu Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val
 20 25 30

Pro Pro Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln
 35 40 45

25 Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile
 50 55 60

30 Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser
 65 70 75

Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu
 80 85 90

35 Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly
 95 100 105

Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu
 110 115 120

40 Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser
 125 130 135

45 Ser Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu
 140 145 150

Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr
 155 160 165

Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln
 170 175 180

5 Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu
 185 190 195

Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg
 200 205 210

10 Gln Met
 212

<210> 15
 15 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 15
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 1 5 10 15

Leu Gly Leu Leu Leu Leu Leu Leu Gly Val Leu Ala Pro Gly Gly
 20 25 30

25 Ala Ser Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln
 35 40 45

Pro Gly Leu Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp
 30 50 55 60

Ser Trp Ile His Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp
 65 70 75

35 Leu Gln Ile Gln Leu His Phe Ala His Thr Gln Gln Gly Asp Leu
 80 85 90

Phe Pro Val Ala His Ile Glu Trp Thr Leu Gln Thr Asp Ala Ser
 95 100 105

40 Ile Leu Tyr Leu Glu Gly Ala Glu Leu Ser Val Leu Gln Leu Asn
 110 115 120

Thr Asn Glu Arg Leu Cys Val Arg Phe Glu Phe Leu Ser Lys Leu
 45 125 130 135

Arg His His His Arg Arg Trp Arg Phe Thr Phe Ser His Phe Val
 140 145 150

Val Asp Pro Asp Gln Glu Tyr Glu Val Thr Val His His Leu Pro
 155 160 165
 5 Lys Pro Ile Pro Asp Gly Asp Pro Asn His Gln Ser Lys Asn Phe
 170 175 180
 Leu Val Pro Asp Cys Glu His Ala Arg Met Lys Val Thr Thr Pro
 185 190 195
 10 Cys Met Ser Ser Gly Ser Leu Trp Asp Pro Asn Ile Thr Val Glu
 200 205 210
 Thr Leu Glu Ala His Gln Leu Arg Val Ser Phe Thr Leu Trp Asn
 15 215 220 225
 Glu Ser Thr His Tyr Gln Ile Leu Leu Thr Ser Phe Pro His Met
 230 235 240
 20 Glu Asn His Ser Cys Phe Glu His Met His His Ile Pro Ala Pro
 245 250 255
 Arg Pro Glu Glu Phe His Gln Arg Ser Asn Val Thr Leu Thr Leu
 260 265 270
 25 Arg Asn Leu Lys Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro
 275 280 285
 Phe Phe Ser Ser Cys Leu Asn Asp Cys Leu Arg His Ser Ala Thr
 30 290 295 300
 Val Ser Cys Pro Glu Met Pro Asp Thr Pro Glu Pro Ile Pro Asp
 305 310 315
 35 Tyr Met Pro Leu Trp
 320

<210> 16

<211> 543

40 <212> DNA

<213> Homo sapiens

<400> 16

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ggcctggggc cctggcccct ggcctcacc aggtgccact ggacctggtg 150

tcacggatga aaccgtatgc ccgcatggag gagtatgaga ggaacatcga 200
 ggagatggtg gccagctga ggaacagctc agagctggcc cagagaaagt 250
 5 gtgaggtcaa cttgcagctg tggatgtcca acaagaggag cctgtctccc 300
 tggggctaca gcatcaacca cgaccccagc cgtatccccg tggacctgcc 350
 10 ggaggcacgg tgccgtgtgc tgggctgtgt gaacccttc accatgcagg 400
 aggaccgcag catggtgagc gtgccggtgt tcagccaggt tcctgtgcgc 450
 cgccgcctct gcccgccacc gcccgccaca gggccttgcc gccagcgcg 500
 15 agtcatggag accatcgctg tgggctgcac ctgcatcttc tga 543

<210> 17

<211> 594

<212> DNA

<213> Homo sapiens

<400> 17

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 cacactgcta ctggctgag gaactgcccc tcggccaggc cccccacac 150
 30 ctgctggctc gaggtgccaa gtggggggcag gctttgcctg tagccctgg 200
 gtccagcctg gaggcagcaa gccacagggg gaggcacgag aggcctcag 250
 ctacgacca gtgcccggctg ctgcggccgg aggaggtgtt ggaggcagac 300
 35 acccaccagc gctccatctc accctggaga taccgtgtgg acacggatga 350
 ggaccgctat ccacagaagc tggccttcgc cgagtgcctg tgcagaggct 400
 40 gtatcgatgc acggacgggc cgcgagacag ctgcgctcaa ctccgtgcgg 450
 ctgctccaga gcctgctggg gctgcgcgc cgccctgct cccgcgacgg 500
 ctcggggctc cccacacctg gggcctttgc cttccacacc gagttcatcc 550
 45 acgtccccgt cggctgcacc tgcgtgctgc cccgttcagt gtga 594

<210> 18

<211> 9
 <212> PRT
 <213> Artificial

5 <220>
 <223> Artificial sequence 1-9

<400> 18
 Gly His His His His His His His His
 10 1 5 9

<210> 19
 <211> 157
 <212> PRT
 15 <213> Homo sapiens

<400> 19
 Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1 5 10 15
 20 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn
 20 25 30
 25 Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp
 35 40 45
 Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser
 50 55 60
 30 Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu
 65 70 75
 Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys
 80 85 90
 35 Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
 95 100 105
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu
 110 115 120
 Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu
 125 130 135
 45 Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val
 140 145 150
 Tyr Phe Gly Ile Ile Ala Leu

155 157

<210> 20
 <211> 21
 5 <212> DNA
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 <220>
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 <400> 20
 ctgtacctcg aggggtgcaga g 21

 <210> 21
 15 <211> 58
 <212> DNA
 <213> Artificial

 <220>
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 <400> 21
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 25 tgtagtcc 58

 <210> 22
 <211> 328
 <212> PRT
 30 <213> Homo sapiens

 <400> 22
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 35 Leu Gly Leu Leu Leu Leu Leu Leu Gly Val Leu Ala Pro Gly Gly
 20 25 30
 Ala Ser Leu Arg Leu Leu Asp His Arg Ala Leu Val Cys Ser Gln
 40 35 40 45
 Pro Gly Leu Asn Cys Thr Val Lys Asn Ser Thr Cys Leu Asp Asp
 50 55 60
 45 Ser Trp Ile His Pro Arg Asn Leu Thr Pro Ser Ser Pro Lys Asp
 65 70 75

	Leu	Gln	Ile	Gln	Leu	His	Phe	Ala	His	Thr	Gln	Gln	Gly	Asp	Leu	
					80					85						90
5	Phe	Pro	Val	Ala	His	Ile	Glu	Trp	Thr	Leu	Gln	Thr	Asp	Ala	Ser	
					95					100						105
	Ile	Leu	Tyr	Leu	Glu	Gly	Ala	Glu	Leu	Ser	Val	Leu	Gln	Leu	Asn	
					110					115						120
10	Thr	Asn	Glu	Arg	Leu	Cys	Val	Arg	Phe	Glu	Phe	Leu	Ser	Lys	Leu	
					125					130						135
	Arg	His	His	His	Arg	Arg	Trp	Arg	Phe	Thr	Phe	Ser	His	Phe	Val	
					140					145						150
15	Val	Asp	Pro	Asp	Gln	Glu	Tyr	Glu	Val	Thr	Val	His	His	Leu	Pro	
					155					160						165
20	Lys	Pro	Ile	Pro	Asp	Gly	Asp	Pro	Asn	His	Gln	Ser	Lys	Asn	Phe	
					170					175						180
	Leu	Val	Pro	Asp	Cys	Glu	His	Ala	Arg	Met	Lys	Val	Thr	Thr	Pro	
					185					190						195
25	Cys	Met	Ser	Ser	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Val	Glu	
					200					205						210
	Thr	Leu	Glu	Ala	His	Gln	Leu	Arg	Val	Ser	Phe	Thr	Leu	Trp	Asn	
					215					220						225
30	Glu	Ser	Thr	His	Tyr	Gln	Ile	Leu	Leu	Thr	Ser	Phe	Pro	His	Met	
					230					235						240
	Glu	Asn	His	Ser	Cys	Phe	Glu	His	Met	His	His	Ile	Pro	Ala	Pro	
35					245					250						255
	Arg	Pro	Glu	Glu	Phe	His	Gln	Arg	Ser	Asn	Val	Thr	Leu	Thr	Leu	
					260					265						270
40	Arg	Asn	Leu	Lys	Gly	Cys	Cys	Arg	His	Gln	Val	Gln	Ile	Gln	Pro	
					275					280						285
	Phe	Phe	Ser	Ser	Cys	Leu	Asn	Asp	Cys	Leu	Arg	His	Ser	Ala	Thr	
					290					295						300
45	Val	Ser	Cys	Pro	Glu	Met	Pro	Asp	Thr	Pro	Glu	Pro	Ile	Pro	Asp	
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<212> PRT
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Ile Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg
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	Val	Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	
20					35					40						45

[illegible]

Ile Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala
95 100 105

Asp Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val
125 130 135

Gln Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile
155 160 165

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 <212> PRT
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<220>
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	Cys	Leu	Ala	His	His	Asp	Pro	Ser	Leu	Arg	Gly	His	Pro	His	Ser
					20					25					30
15	His	Gly	Thr	Pro	His	Cys	Tyr	Ser	Ala	Glu	Glu	Leu	Pro	Leu	Gly
					35					40					45
	Gln	Ala	Pro	Pro	His	Leu	Leu	Ala	Arg	Gly	Ala	Lys	Trp	Gly	Gln
20					50					55					60
	Ala	Leu	Pro	Val	Ala	Leu	Val	Ser	Ser	Leu	Glu	Ala	Ala	Ser	His
					65					70					75
25	Arg	Gly	Arg	His	Glu	Arg	Pro	Ser	Ala	Thr	Thr	Gln	Cys	Pro	Val
					80					85					90
	Leu	Arg	Pro	Glu	Glu	Val	Leu	Glu	Ala	Asp	Thr	His	Gln	Arg	Ser
					95					100					105
30	Ile	Ser	Pro	Trp	Arg	Tyr	Arg	Val	Asp	Thr	Asp	Glu	Asp	Arg	Tyr
					110					115					120
	Pro	Gln	Lys	Leu	Ala	Phe	Ala	Glu	Cys	Leu	Cys	Arg	Gly	Cys	Ile
35					125					130					135
	Asp	Ala	Arg	Thr	Gly	Arg	Glu	Thr	Ala	Ala	Leu	Asn	Ser	Val	Arg
					140					145					150
40	Leu	Leu	Gln	Ser	Leu	Leu	Val	Leu	Arg	Arg	Arg	Pro	Cys	Ser	Arg
					155					160					165
	Asp	Gly	Ser	Gly	Leu	Pro	Thr	Pro	Gly	Ala	Phe	Ala	Phe	His	Thr
					170					175					180
45	Glu	Phe	Ile	His	Val	Pro	Val	Gly	Cys	Thr	Cys	Val	Leu	Pro	Arg
					185					190					195

10	Met	Ala	Lys	Val	Pro	Asp	Met	Phe	Glu	Asp	Leu	Lys	Asn	Cys	Tyr
	1				5					10					15
	Ser	Glu	Asn	Glu	Glu	Asp	Ser	Ser	Ser	Ile	Asp	His	Leu	Ser	Leu
					20					25					30
15	Asn	Gln	Lys	Ser	Phe	Tyr	His	Val	Ser	Tyr	Gly	Pro	Leu	His	Glu
					35					40					45
	Gly	Cys	Met	Asp	Gln	Ser	Val	Ser	Leu	Ser	Ile	Ser	Glu	Thr	Ser
20					50					55					60
	Lys	Thr	Ser	Lys	Leu	Thr	Phe	Lys	Glu	Ser	Met	Val	Val	Val	Ala
					65					70					75
25	Thr	Asn	Gly	Lys	Val	Leu	Lys	Lys	Arg	Arg	Leu	Ser	Leu	Ser	Gln
					80					85					90
	Ser	Ile	Thr	Asp	Asp	Asp	Leu	Glu	Ala	Ile	Ala	Asn	Asp	Ser	Glu
					95					100					105
30	Glu	Glu	Ile	Ile	Lys	Pro	Arg	Ser	Ala	Pro	Phe	Ser	Phe	Leu	Ser
					110					115					120
	Asn	Val	Lys	Tyr	Asn	Phe	Met	Arg	Ile	Ile	Lys	Tyr	Glu	Phe	Ile
35					125					130					135
	Leu	Asn	Asp	Ala	Leu	Asn	Gln	Ser	Ile	Ile	Arg	Ala	Asn	Asp	Gln
					140					145					150
40	Tyr	Leu	Thr	Ala	Ala	Ala	Leu	His	Asn	Leu	Asp	Glu	Ala	Val	Lys
					155					160					165
	Phe	Asp	Met	Gly	Ala	Tyr	Lys	Ser	Ser	Lys	Asp	Asp	Ala	Lys	Ile
					170					175					180
45	Thr	Val	Ile	Leu	Arg	Ile	Ser	Lys	Thr	Gln	Leu	Tyr	Val	Thr	Ala
					185					190					195

5

10

15

20

30

35

40

45

10	Val	Met	Val	Thr	Leu	Phe	Tyr	Phe	Gln	Glu	Asp	Glu
					170					175		177